

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Fri Oct 19 12:10:42 EDT 2007

=====

Application No: 09925284 Version No: 7.0

Input Set:

Output Set:

Started: 2007-10-03 14:47:01.332
Finished: 2007-10-03 14:47:01.875
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 543 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)

SEQUENCE LISTING

<110> Hawiger, Daniel
Steinman, Ralph M.
Nussenzweig, Michel C.

<120> Enhanced Antigen Delivery and Modulation
of the Immune Response Therefrom

<130> RUJ-001CNCPRCE2

<140> 09925284
<141> 2001-08-09

<150> 09/586, 704
<151> 2000-06-05

<150> 08/381, 528
<151> 1995-01-31

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1
atagtttagc ggccgcgata tctcaactaac actcattctt gttgaagct 49

<210> 2
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 2
tcttctcaga gagggtgaga ggaccatttc gatcgatcac tcgccccgca tttgata 57

<210> 3
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 3

ctagcgacat ggccaagaag gagacagtct ggaggctcga ggagttcggt aggttcacaa 60
acaggaac 68

<210> 4
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 4
acagacggta gcacagacta tggattctc cagattaaca gcaggtatta tgacggtagg 60
acatgatagg c 71

<210> 5
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 5
gtctgtgttc ctgtttgtga acctaccgaa ctccctcgagc ctccagactg tctccttctt 60
ggccatgtcg 70

<210> 6
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 6
ggccgcctat catgtcctac cgtcataata cctgctgtta atctggagaa taccatagtc 60
tgtgctacc 69

<210> 7
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<223> carboxy terminal DEC-205

<400> 7
Arg His Arg Leu His Leu Ala Gly Phe Ser Ser Val Arg Tyr Ala Gln
1 5 10 15
Gly Val Asn Glu Asp Glu Ile Met Leu Pro Ser Phe His Asp
20 25 30

<210> 8
<211> 25
<212> PRT

Glu Thr Trp Tyr His Asp Cys Ile His Asp Glu Asp His Ser Gly Pro
180 185 190
Trp Cys Ala Thr Thr Leu Ser Tyr Glu Tyr Asp Gln Lys Trp Gly Ile
195 200 205
Cys Leu Leu Pro Glu Ser Gly Cys Glu Gly Asn Trp Glu Lys Asn Glu
210 215 220
Gln Ile Gly Ser Cys Tyr Gln Phe Asn Asn Gln Glu Ile Leu Ser Trp
225 230 235 240
Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
245 250 255
Ile His Ser Ala Ala Glu Leu Ala Tyr Ile Thr Gly Lys Glu Asp Ile
260 265 270
Ala Arg Leu Val Trp Leu Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
275 280 285
Trp Glu Trp Ser Asp Phe Arg Pro Leu Lys Phe Leu Asn Trp Asp Pro
290 295 300
Gly Thr Pro Val Ala Pro Val Ile Gly Gly Ser Ser Cys Ala Arg Met
305 310 315 320
Asp Thr Glu Ser Gly Leu Trp Gln Ser Val Ser Cys Glu Ser Gln Gln
325 330 335
Pro Tyr Val Cys Lys Lys Pro Leu Asn Asn Thr Leu Glu Leu Pro Asp
340 345 350
Val Trp Thr Tyr Thr Asp Thr His Cys His Val Gly Trp Leu Pro Asn
355 360 365
Asn Gly Phe Cys Tyr Leu Leu Ala Asn Glu Ser Ser Trp Asp Ala
370 375 380
Ala His Leu Lys Cys Lys Ala Phe Gly Ala Asp Leu Ile Ser Met His
385 390 395 400
Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Gly Asp
405 410 415
Val Lys Lys Glu Ile Trp Thr Gly Leu Lys Asn Thr Asn Ser Pro Ala
420 425 430
Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asn
435 440 445
Glu Asn Glu Pro Ser Val Pro Phe Asn Lys Thr Pro Asn Cys Val Ser
450 455 460
Tyr Leu Gly Lys Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Lys Lys
465 470 475 480
Leu Arg Tyr Val Cys Lys Lys Gly Glu Ile Thr Lys Asp Ala Glu
485 490 495
Ser Asp Lys Leu Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
500 505 510
Thr Cys Tyr Lys Ile Tyr Glu Lys Glu Ala Pro Phe Gly Thr Asn Cys
515 520 525
Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Phe Leu Asn Tyr Met
530 535 540
Met Lys Asn Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
545 550 555 560
Arg Asp Pro Asp Ser Arg Gly Glu Tyr Ser Trp Ala Val Ala Gln Gly
565 570 575
Val Lys Gln Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
580 585 590
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Thr Leu Gly Lys
595 600 605
Trp Glu Val Lys Asn Cys Arg Ser Phe Arg Ala Leu Ser Ile Cys Lys
610 615 620
Lys Val Ser Glu Pro Gln Glu Pro Glu Glu Ala Ala Pro Lys Pro Asp

625 630 635 640
Asp Pro Cys Pro Glu Gly Trp His Thr Phe Pro Ser Ser Leu Ser Cys
645 650 655
Tyr Lys Val Phe His Ile Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
660 665 670
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Pro Ser Phe
675 680 685
Ser Arg Arg Glu Glu Ile Lys Asp Phe Val His Leu Leu Lys Asp Gln
690 695 700
Phe Ser Gly Gln Arg Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
705 710 715 720
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Ala
725 730 735
Val Met Met Glu Pro Glu Phe Gln Gln Asp Phe Asp Ile Arg Asp Cys
740 745 750
Ala Ala Ile Lys Val Leu Asp Val Pro Trp Arg Arg Val Trp His Leu
755 760 765
Tyr Glu Asp Lys Asp Tyr Ala Tyr Trp Lys Pro Phe Ala Cys Asp Ala
770 775 780
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Ser Thr Pro Gln Met
785 790 795 800
Pro Asp Trp Tyr Asn Pro Glu Arg Thr Gly Ile His Gly Pro Pro Val
805 810 815
Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Pro His Leu Asn
820 825 830
Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
835 840 845
Thr Ile Thr Ser Phe Thr Gly Leu Lys Ala Ile Lys Asn Lys Leu Ala
850 855 860
Asn Ile Ser Gly Glu Glu Gln Lys Trp Trp Val Lys Thr Ser Glu Asn
865 870 875 880
Pro Ile Asp Arg Tyr Phe Leu Gly Ser Arg Arg Arg Leu Trp His His
885 890 895
Phe Pro Met Thr Phe Gly Asp Glu Cys Leu His Met Ser Ala Lys Thr
900 905 910
Trp Leu Val Asp Leu Ser Lys Arg Ala Asp Cys Asn Ala Lys Leu Pro
915 920 925
Phe Ile Cys Glu Arg Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro
930 935 940
Asp Pro Ala Ala Lys Val Gln Cys Thr Glu Lys Trp Ile Pro Phe Gln
945 950 955 960
Asn Lys Cys Phe Leu Lys Val Asn Ser Gly Pro Val Thr Phe Ser Gln
965 970 975
Ala Ser Gly Ile Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu
980 985 990
Ser Arg Gly Glu Gln Asp Phe Ile Ile Ser Leu Leu Pro Glu Met Glu
995 1000 1005
Ala Ser Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Arg Ile Asn
1010 1015 1020
Arg Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro Leu
1025 1030 1035 1040
Leu Val Gly Arg Arg Leu Ser Ile Pro Thr Asn Phe Phe Asp Asp Glu
1045 1050 1055
Ser His Phe His Cys Ala Leu Ile Leu Asn Leu Lys Lys Ser Pro Leu
1060 1065 1070
Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg His Ser Leu Ser
1075 1080 1085

Leu Cys Gln Lys Tyr Ser Glu Thr Glu Asp Gly Gln Pro Trp Glu Asn
1090 1095 1100
Thr Ser Lys Thr Val Lys Tyr Leu Asn Asn Leu Tyr Lys Ile Ile Ser
1105 1110 1115 1120
Lys Pro Leu Thr Trp His Gly Ala Leu Lys Glu Cys Met Lys Glu Lys
1125 1130 1135
Met Arg Leu Val Ser Ile Thr Asp Pro Tyr Gln Gln Ala Phe Leu Ala
1140 1145 1150
Val Gln Ala Thr Leu Arg Asn Ser Ser Phe Trp Ile Gly Leu Ser Ser
1155 1160 1165
Gln Asp Asp Glu Leu Asn Phe Gly Trp Ser Asp Gly Lys Arg Leu Gln
1170 1175 1180
Phe Ser Asn Trp Ala Gly Ser Asn Glu Gln Leu Asp Asp Cys Val Ile
1185 1190 1195 1200
Leu Asp Thr Asp Gly Phe Trp Lys Thr Ala Asp Cys Asp Asp Asn Gln
1205 1210 1215
Pro Gly Ala Ile Cys Tyr Tyr Pro Gly Asn Glu Thr Glu Glu Val
1220 1225 1230
Arg Ala Leu Asp Thr Ala Lys Cys Pro Ser Pro Val Gln Ser Thr Pro
1235 1240 1245
Trp Ile Pro Phe Gln Asn Ser Cys Tyr Asn Phe Met Ile Thr Asn Asn
1250 1255 1260
Arg His Lys Thr Val Thr Pro Glu Glu Val Gln Ser Thr Cys Glu Lys
1265 1270 1275 1280
Leu His Pro Lys Ala His Ser Leu Ser Ile Arg Asn Glu Glu Glu Asn
1285 1290 1295
Thr Phe Val Val Glu Gln Leu Leu Tyr Phe Asn Tyr Ile Ala Ser Trp
1300 1305 1310
Val Met Leu Gly Ile Thr Tyr Glu Asn Asn Ser Leu Met Trp Phe Asp
1315 1320 1325
Lys Thr Ala Leu Ser Tyr Thr His Trp Arg Thr Gly Arg Pro Thr Val
1330 1335 1340
Lys Asn Gly Lys Phe Leu Ala Gly Leu Ser Thr Asp Gly Phe Trp Asp
1345 1350 1355 1360
Ile Gln Ser Phe Asn Val Ile Glu Glu Thr Leu His Phe Tyr Gln His
1365 1370 1375
Ser Ile Ser Ala Cys Lys Ile Glu Met Val Asp Tyr Glu Asp Lys His
1380 1385 1390
Asn Gly Thr Leu Pro Gln Phe Ile Pro Tyr Lys Asp Gly Val Tyr Ser
1395 1400 1405
Val Ile Gln Lys Lys Val Thr Trp Tyr Glu Ala Leu Asn Ala Cys Ser
1410 1415 1420
Gln Ser Gly Gly Glu Leu Ala Ser Val His Asn Pro Asn Gly Lys Leu
1425 1430 1435 1440
Phe Leu Glu Asp Ile Val Asn Arg Asp Gly Phe Pro Leu Trp Val Gly
1445 1450 1455
Leu Ser Ser His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly
1460 1465 1470
Arg Ala Phe Asp Tyr Val Pro Trp Gln Ser Leu Gln Ser Pro Gly Asp
1475 1480 1485
Cys Val Val Leu Tyr Pro Lys Gly Ile Trp Arg Arg Glu Lys Cys Leu
1490 1495 1500
Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Asp Lys Lys
1505 1510 1515 1520
Leu Ile Phe His Val Lys Ser Ser Lys Cys Pro Val Ala Lys Arg Asp
1525 1530 1535
Gly Pro Gln Trp Val Gln Tyr Gly His Cys Tyr Ala Ser Asp Gln

1540	1545	1550
Val Leu His Ser Phe Ser Glu Ala Lys Gln Val Cys Gln Glu Leu Asp		
1555	1560	1565
His Ser Ala Thr Val Val Thr Ile Ala Asp Glu Asn Glu Asn Lys Phe		
1570	1575	1580
Val Ser Arg Leu Met Arg Glu Asn Tyr Asn Ile Thr Met Arg Val Trp		
1585	1590	1595
Leu Gly Leu Ser Gln His Ser Leu Asp Gln Ser Trp Ser Trp Leu Asp		
1605	1610	1615
Gly Leu Asp Val Thr Phe Val Lys Trp Glu Asn Lys Thr Lys Asp Gly		
1620	1625	1630
Asp Gly Lys Cys Ser Ile Leu Ile Ala Ser Asn Glu Thr Trp Arg Lys		
1635	1640	1645
Val His Cys Ser Arg Gly Tyr Ala Arg Ala Val Cys Lys Ile Pro Leu		
1650	1655	1660
Ser Pro Asp Tyr Thr Gly Ile Ala Ile Leu Phe Ala Val Leu Cys Leu		
1665	1670	1675
Leu Gly Leu Ile Ser Leu Ala Ile Trp Phe Leu Leu Gln Arg Ser His		
1685	1690	1695
Ile Arg Trp Thr Gly Phe Ser Ser Val Arg Tyr Glu His Gly Thr Asn		
1700	1705	1710
Glu Asp Glu Val Met Leu Pro Ser Phe His Asp		
1715	1720	